



## SEQUENCE LISTING

<110> Gray, Jeff

Valkirs, Gunars E.

Buechler, Joe

Biosite Diagnostics

<120> Diagnostic Assays for Detection of Cryptosporidium  
parvum

<130> 014907-001900US

<140> 09/158,180

<141> 1998-09-21

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 1446

---

<212> DNA

<213> Cryptosporidium parvum

<220>

<221> CDS

<222> (1) .. (1446)

<223> C. parvum protein disulfide isomerase (PDI) cDNA  
of Applicants

&lt;400&gt; 1

atg atc gga att aga agc ttg gtt tca gca gca ttt tta ggt ttt tct 48

Met Ile Gly Ile Arg Ser Leu Val Ser Ala Ala Phe Leu Gly Phe Ser

1

5

10

15

tgt ctc tcc aag gta gtc ttg ggt gga gat gaa gct cac ttc att tca 96

Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser

20

25

30

gaa cac att act tcc tta act tcc tcc aac ttc gaa gac ttc att aag 144

Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys

35

40

45

agc aag gaa cac gta att gtt act ttc ttt gcc cca tgg tgc ggc cat 192

Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His

50

55

60

tgt act gct tta gag cca gaa ttc aag gca aca tgc gct gaa atc tca 240

Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser

65

70

75

80

~~aag ctc tct ccc cca gta cac tgt ggc agt gtt gat gca act gaa aat 288~~

Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn

85

90

95

atg gag ctt gca caa caa tat ggt gtg agc gga tac cca acc atc aaa 336

Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys

100

105

110

ttc ttc agt ggt att gac agt gtt cag aac tat tca gga gca aga agc 384

Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser

115

120

125

aag gat gca ttc atc aag tat att aag aag ttg acc gga cca gca gtc 432

Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val

130

135

140

caa gtt gct gaa tca gaa gaa gct atc aag aca atc ttc gct tct tct 480

Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser

145

150

155

160

tct tca gcc ttt gtt gga aga ttc acc tct aag gac tca gct gag tat 528

Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr

165

170

175

gct gtc ttc gag aag gtt gct agt ggt cac cgc gag cac aac tat gct 576

Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala

180

185

190

ttc att gct ttc ttc caa gaa ggt gaa caa aag ctc gag gta tta cac 624

Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His

195

200

205

aag gac gag gag cca gtt tct ctc cca atg cca aag act gtt gaa gag 672

Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu

210

215

220

ttg gag gcc aag ata tcc ata atg aat gta cca ttg ttc tct gca att 720

Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile

225

230

235

240

agt gct gag aac tac tcc ctc tat atg tca aga gaa ggt tat act gcc 768

Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala

245

250

255

tgg ttc tgt ggt act aac gag gac ttc gcc aag tat gct tca aac att 816

Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile

260

265

270

aga aag gtt gca gct gat tac aga gaa aag tat gcc ttt gtt ttc ctt 864

Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu

275

280

285

gat act gag caa ttt ggt tcc cat gct act caa cat ctc tta att gag 912

Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu

290

295

300

aaa ttc cca ggt ttg gtt atc caa agt gtc aat gtt cca tca att aga 960

Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg

305

310

315

320

tac atg tat ggt cca gct aaa ttc gac tct gtt gag cca tta aag gaa 1008

~~Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu~~

325

330

335

ttt atg aag caa gtt tct gaa ggc aag cac gaa ctc agc att aag tct 1056

Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser

340

345

350

gag cca atc cca gct gag caa tct ggt cca gtc act gtt gtt gtt ggt 1104

Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly

355

360

365

aag acc ttc gaa gaa att gtt ttc aga agt gac aag gat gtt ctt ttg 1152

Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu

370

375

380

gaa atc tat gcc caa tgg tgt gga cac tgt aag aac ctc gag cca atc 1200

Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile

385

390

395

400

tac aac caa ctc ggc gaa gag tac aag gac aac gac aag gtt gtg att 1248

Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile

405

410

415

gca aag atc aat gga cca caa aac gat atc cca tat gaa ggt ttc agt 1296

Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser

420

425

430

cca aga gcc ttc cca act atc ttg ttc gtc aag gcc gga act aga acc 1344

Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr

435

440

445

cca att cct tat gat gga aag aga act gtt gag gcc ttc aag gaa ttc 1392

~~Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe~~

450

455

460

atc agt gaa cat tct tcc ttc cct caa gaa aag gaa tct cgt gac gaa 1440

Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu

465

470

475

480

ctc taa

1446

Leu

<210> 2

<211> 481

<212> PRT

<213> Cryptosporidium parvum

<400> 2

Met Ile Gly Ile Arg Ser Leu Val Ser Ala Ala Phe Leu Gly Phe Ser

1 5 10 15

Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser

20 25 30

Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys

35 40 45

Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His

50 55 60

Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser

65 70 75 80

---

Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn

85 90 95

Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys

100 105 110

Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser

115 120 125

Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val  
 130 135 140

Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser  
 145 150 155 160

Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr  
 165 170 175

Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala  
 180 185 190

Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His  
 195 200 205

Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu  
 210 215 220

Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile  
 225 230 235 240

---

~~Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala~~  
 245 250 255

Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile  
 260 265 270

Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu  
 275 280 285

Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu  
 290 295 300

Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg  
 305 310 315 320

Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu  
 325 330 335

Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser  
 340 345 350

Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly  
 355 360 365

Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu  
 370 375 380

Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile  
 385 390 395 400

~~Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile~~  
 405 410 415

Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser  
 420 425 430

Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr  
 435 440 445



Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe

450

455

460

Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu

465

470

475

480

Leu

<210> 3

<211> 32

<212> PRT

<213> *Cryptosporidium parvum*

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> 32 amino acid region for *C. parvum* protein

disulfide isomerase (PDI) of Applicants differing

from Blunt et al. (1996) Gene 181:221-223; GenBank

Accession No. U48261

<400> 3

Ala Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn

1

5

10

15

Ile Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe

20

25

30

<210> 4

<211> 41

<212> PRT

<213> Cryptosporidium parvum

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> positions 250-290 of C. parvum protein disulfide  
isomerase (PDI) according to Blunt et al. (1996)  
Gene 181:221-223; GenBank Accession No. U48261

<220>

<221> PEPTIDE

<222> (7)..(38)

<223> 32 amino acid region of C. parvum protein  
disulfide isomerase (PDI) of Blunt et al. that  
differs from that of Applicant PDI

<400> 4

Ser Arg Glu Gly Tyr Thr Pro Gly Ser Val Val Leu Thr Arg Thr Ser

1

5

10

15

Pro Ser Met Leu Gln Thr Leu Glu Arg Leu Gln Leu Ile Thr Glu Lys

20

25

30

Ser Met Pro Leu Phe Ser Leu Asp Thr

35

40

<210> 5

<211> 41

<212> PRT

<213> Cryptosporidium parvum

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> positions 250-290 (numbering convention used by  
Blunt et al.) of C. parvum protein disulfide  
isomerase (PDI) of the Applicants

<220>

<221> PEPTIDE

<222> (7)..(38)

<223> 32 amino acid region of C. parvum protein  
disulfide isomerase (PDI) from Applicants that  
differs from Blunt et al. PDI

<400> 5

Ser Arg Glu Gly Tyr Thr Ala Trp Phe Cys Gly Thr Asn Glu Asp Phe

---

1

5

10

15

Ala Lys Tyr Ala Ser Asn Ile Arg Lys Val Ala Ala Asp Tyr Arg Glu

20

25

30

Lys Tyr Ala Phe Val Phe Leu Asp Thr

35

40

<210> 6

<211> 23

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer A

<400> 6

gtaaaacgac ggccagtgaa ttg

23

<210> 7

<211> 54

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer B

<400> 7

---

accggttttt ttggatggag tgaaacgatg atcggaattc gtagcttggt ttca

54

<210> 8

<211> 89

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer C

<400> 8

gtgataaaact accgcattaa agcttatcga tgataagctg tcaattagtg atggatgatgg 60

tgatggagtt cgtcacgaga ttccttttc

89

<210> 9

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer D

<400> 9

tccaaggtag tcttgggtgg

20

<210> 10

<211> 20

<212> DNA

---

<213> Cryptosporidium parvum

<220>

<223> primer E

<400> 10

aagctctctc ccccagtaca

20

<210> 11

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer F

<400> 11

gcagtcacaag ttgctgaatc

20

<210> 12

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer G

<400> 12

---

ctcgagggtat tacacaagga

20

<210> 13

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer H

<400> 13

ccaagtatgc ttcaaacatt

20

<210> 14

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer I

<400> 14

ttcgactctg ttgagccatt

20

<210> 15

<211> 21

<212> DNA

<213> Cryptosporidium parvum

<220>

---

<223> primer J

<400> 15

tgtggacact gtaagaacct c

21

<210> 16

<211> 18

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer K

<400> 16

gaggatgacg atgagcgc

18

<210> 17

<211> 21

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer L

<400> 17

gcaactctct actgtttctc c

21

<210> 18

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer M



<400> 18

tcgctgccca accagccatg

20

<210> 19

<211> 75

<212> DNA

<213> *Cryptosporidium parvum*

<220>

<223> primer N

<400> 19

gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atggatgatgg 60

tgatgacaat ccctg

75

---